a) hybridizing a plurality of nucleic acid probes with said target nucleic acid, wherein said probes are complementary to different overlapping regions of said control nucleic acid;

b) determining the melting temperature (T_m) of at least two overlapping probes from said target nucleic acid;

c) determining for each of said at least two probes the difference between the T_m of said target nucleic acid and each of said at least two probes and the T_m of said control nucleic acid and each of said at least two probes thus determining the ΔT_m for each of said at least two probes; and

d) determining the difference in determined ΔT_m between overlapping probes as an indication of the presence or absence of a sequence alteration in said target nucleic acid as compared to said control nucleic acid.

6. (Amended) A method of identifying a sequence alteration in a target nucleic acid as compared to a control nucleic acid, said method comprising:

a) hybridizing a plurality of nucleic acid probes with said target nucleic acid, wherein a first set of probes is complementary to regions of said control nucleic acid separated by one or more nucleotides and at least a second set of probes is complementary to regions of said control separated by one or more nucleotides, wherein the regions complementary to said second set of probes include the nucleic acids separating the first set of probes and are overlapping with the regions complementary to said first set of probes;

b) determining the melting temperature (T_m) of at least two overlapping probes from said target nucleic acid;

c) determining for each of said at least two overlapping probes the difference between the T_m of said target nucleic acid and each of said at least two overlapping probes and the T_m of said control nucleic acid and each of said at least two overlapping probes thus determining the ΔT_m for each of said at least two overlapping probes; and